



#15

SEQUENCE LISTING

<110> Feder, J.
Mintier, G.
Ramanathan, C.
Hawken, D.
Cacace, A.
Barber, L.
Kornacker, M.

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY6, EXPRESSED
HIGHLY IN SMALL INTESTINE

<130> D0040 NP

<140> 09/966,422

<141> 2001-09-26

<150> 60/235,602

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<170> PatentIn version 3.2

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His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
180 185 190

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195 200 205

Val Thr Gly Leu Ala Leu Thr Val Ile Phe Gln Ile Val Thr Arg Lys
210 215 220

Val Arg Lys Thr Ser Val Thr Trp Val Leu Val Asn Leu Cys Ile Ser
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Thr Met Lys Pro Leu Pro Arg His Phe Ile Leu Phe Ile Ser Leu Ile
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Ser Tyr Ile Phe Cys Leu Phe Asn Thr Thr Gln Gly Leu Gln Ile Phe
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aaattctttt acaagttact ataaaggaca caaagagaaa actttacctt ccagaacaaa	360

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Asp Val Ile Met Ile Glu Ser Ala Asn Tyr Gly Arg Thr Asp Asp Lys
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Ile Cys Asp Ser Asp Pro Ala Gln Met Glu Asn Ile Arg Cys Tyr Leu
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Pro Asp Ala Tyr Lys Ile Met Ser Gln Arg Cys Asn Asn Arg Thr Gln
85 90 95

Cys Ala Val Val Ala Gly Pro Asp Val Phe Pro Asp Pro Cys Pro Gly
100 105 110

Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Glu Cys Val Pro Tyr Lys Val
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Glu Gln Lys Val Phe Leu Cys Pro Gly Leu Leu Lys Gly Val Tyr Gln
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Ser Glu His Leu Phe Glu Ser Asp His Gln Ser Gly Ala Trp Cys Lys
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Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ser Ser Lys Asp Asp Phe Ile
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Ala Gly Arg Pro Thr Thr Thr Tyr Lys Leu Pro His Arg Val Asp Gly
195 200 205

Thr Gly Phe Val Val Tyr Asp Gly Ala Leu Phe Phe Asn Lys Glu Arg
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Thr Arg Asn Ile Val Lys Phe Asp Leu Arg Thr Arg Ile Lys Ser Gly
225 230 235 240

Glu Ala Ile Ile Ala Asn Ala Asn Tyr His Asp Thr Ser Pro Tyr Arg
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Trp Gly Gly Lys Ser Asp Ile Asp Leu Ala Val Asp Glu Asn Gly Leu
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Asn Lys Ile Asp Tyr Ile Tyr Asn Thr Asp Gln Ser Lys Asp Ser Leu
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370 375 380

Val Lys Tyr Ser Leu Asp Phe Gly Pro Leu Asp Ser Arg Ser Gly Pro
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Val His His Gly Gln Val Ser Tyr Ile Ser Pro Pro Ile His Leu Asp
405 410 415

Ser Asp Leu Glu Arg Pro Pro Val Arg Gly Ile Ser Thr Thr Gly Pro
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Trp Asn Leu Gly Arg Ser Thr Thr Pro Ser Leu Pro Gly Arg Arg Asn
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Thr His Leu Pro Ser Ala Ala Ser Gln Ile Pro Ala Met Glu Glu Ser

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Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr Asn Asn Leu Gly Pro
740 745 750

Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu Gly Thr Glu Ala Met
755 760 765

Ser Thr Asn His Ser Val Ile Val Asn Ser Pro Val Ile Thr Ala Ala
770 775 780

Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu Ala Asp Pro Val Val
785 790 795 800

Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn Phe Asn Pro Asn
805 810 815

Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
820 825 830

Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
835 840 845

Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
850 855 860

Val Lys His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr
865 870 875 880

Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe
885 890 895

Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His
900 905 910

Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile
915 920 925

Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala Val Phe Ala Ala
930 935 940

Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu
 945 950 955 960

Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His
 965 970 975

Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu
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Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp
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Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe
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Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val Ile Phe Leu
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Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile Leu Lys
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Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile Gly
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Thr Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His
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Gly Ser Gln Ser Arg Ile Arg Arg Met Trp Asn Asp Thr Val Arg
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Lys Gln Ser Glu Ser Ser Phe Ile Thr Gly Asp Ile Asn Ser Ser
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Ala Ser Leu Asn Arg Glu Pro Tyr Arg Glu Thr Ser Met Gly Val
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Gly Tyr Lys Cys His Gly Tyr Ser Thr Thr Glu Trp
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Leu Leu Gln Gln Pro Ala Ala Glu Arg Ser Thr Ala His Arg Gly Gln
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Gly Pro Arg Gly Thr Ala Arg Gly Val Arg Gly Pro Gly Ala Pro Gly
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Ala Gln Ile Ala Ala Gln Ala Phe Ser Arg Ala Pro Ile Pro Met Ala
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Val Val Arg Arg Glu Leu Ser Cys Glu Ser Tyr Pro Ile Glu Leu Arg
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Cys Pro Gly Thr Asp Val Ile Met Ile Glu Ser Ala Asn Tyr Gly Arg
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Asn Arg Thr Gln Cys Ala Val Val Ala Gly Pro Asp Val Phe Pro Asp
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Pro Cys Pro Gly Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Glu Cys Val
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Pro Tyr Lys Val Glu Gln Lys Val Phe Leu Cys Pro Gly Leu Leu Lys
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Gly Val Tyr Gln Ser Glu His Leu Phe Glu Ser Asp His Gln Ser Gly
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Ala Trp Cys Lys Asp Pro Leu Gln Ala Ser Asp Lys Ile Tyr Tyr Met
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Pro Trp Thr Pro Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ser Ser Lys
 245 250 255

Asp Asp Phe Ile Ala Gly Arg Pro Thr Thr Tyr Lys Leu Pro His
 260 265 270

Arg Val Asp Gly Thr Gly Phe Val Val Tyr Asp Gly Ala Leu Phe Phe
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Asn Lys Glu Arg Thr Arg Asn Ile Val Lys Phe Asp Leu Arg Thr Arg
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Ile Lys Ser Gly Glu Ala Ile Ile Ala Asn Ala Asn Tyr His Asp Thr
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Ser Pro Tyr Arg Trp Gly Gly Lys Ser Asp Ile Asp Leu Ala Val Asp
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Glu Asn Gly Leu Trp Val Ile Tyr Ala Thr Glu Gln Asn Asn Gly Lys
 340 345 350

Ile Val Ile Ser Gln Leu Asn Pro Tyr Thr Leu Arg Ile Glu Gly Thr
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Trp Asp Thr Ala Tyr Asp Lys Arg Ser Ala Ser Asn Ala Phe Met Ile
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Cys Gly Ile Leu Tyr Val Val Lys Ser Val Tyr Glu Asp Asp Asp Asn
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Glu Ala Thr Gly Asn Lys Ile Asp Tyr Ile Tyr Asn Thr Asp Gln Ser
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Lys Asp Ser Leu Val Asp Val Pro Phe Pro Asn Ser Tyr Gln Tyr Ile
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Ala Ala Val Asp Tyr Asn Pro Arg Asp Asn Leu Leu Tyr Val Trp Asn
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Asn Tyr His Val Val Lys Tyr Ser Leu Asp Phe Gly Pro Leu Asp Ser
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Arg Ser Gly Pro Val His His Gly Gln Val Ser Tyr Ile Ser Pro Pro
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Ile His Leu Asp Ser Asp Leu Glu Arg Pro Pro Val Arg Gly Ile Ser
 485 490 495

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Arg Thr Thr Thr Trp Asn Leu Gly Arg Ser Thr Thr Pro Ser Leu Pro
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Leu Asp Val Thr Thr His Leu Pro Ser Ala Ala Ser Gln Ile Pro Ala
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 595 600 605

Pro Gln Gly Pro Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His
 610 615 620

Ile Thr Gln Lys Leu Lys Ser Gly Glu Thr Ala Ala Asn Ile Ala Arg
 625 630 635 640

Glu Leu Ala Glu Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr
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Tyr Ser Val Arg Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln
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Leu Arg Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu
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Asn Lys Leu Gln Lys Arg Glu Arg Ser Cys Arg Ala Tyr Val Gln Ala
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Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn Ala
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Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met Leu
 725 730 735

Leu Asp Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu Leu
 740 745 750

Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Gln Leu Glu Val
 755 760 765

Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro Glu
 770 775 780

Asn Thr Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu Lys
 785 790 795 800

Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr Asn

805	810	815
Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu Gly		
820	825	830
Thr Glu Ala Met Ser Thr Asn His Ser Val Ile Val Asn Ser Pro Val		
835	840	845
Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu Ala		
850	855	860
Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn		
865	870	875
Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr		
885	890	895
Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr		
900	905	910
His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met		
915	920	925
Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu Leu		
930	935	940
Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu		
945	950	955
Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg		
965	970	975
Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu		
980	985	990
Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala		
995	1000	1005
Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr		
1010	1015	1020
Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu		
1025	1030	1035

Val	Phe	Glu	Ser	Glu	His	Ser	Arg	Arg	Lys	Tyr	Phe	Tyr	Leu	Val
1040						1045					1050			
Gly	Tyr	Gly	Met	Pro	Ala	Leu	Ile	Val	Ala	Val	Ser	Ala	Ala	Val
1055						1060					1065			
Asp	Tyr	Arg	Ser	Tyr	Gly	Thr	Asp	Lys	Val	Cys	Trp	Leu	Arg	Leu
1070						1075					1080			
Asp	Thr	Tyr	Phe	Ile	Trp	Ser	Phe	Ile	Gly	Pro	Ala	Thr	Leu	Ile
1085						1090					1095			
Ile	Met	Leu	Asn	Val	Ile	Phe	Leu	Gly	Ile	Ala	Leu	Tyr	Lys	Met
1100						1105					1110			
Phe	His	His	Thr	Ala	Ile	Leu	Lys	Pro	Glu	Ser	Gly	Cys	Leu	Asp
1115						1120					1125			
Asn	Ile	Lys	Ser	Trp	Val	Ile	Gly	Ala	Ile	Ala	Leu	Leu	Cys	Leu
1130						1135					1140			
Leu	Gly	Leu	Thr	Trp	Ala	Phe	Gly	Leu	Met	Tyr	Ile	Asn	Glu	Ser
1145						1150					1155			
Thr	Val	Ile	Met	Ala	Tyr	Leu	Phe	Thr	Ile	Phe	Asn	Ser	Leu	Gln
1160						1165					1170			
Gly	Met	Phe	Ile	Phe	Ile	Phe	His	Cys	Val	Leu	Gln	Lys	Lys	Val
1175						1180					1185			
Arg	Lys	Glu	Tyr	Gly	Lys	Cys	Leu	Arg	Thr	His	Cys	Cys	Ser	Gly
1190						1195					1200			
Lys	Ser	Thr	Glu	Ser	Ser	Ile	Gly	Ser	Gly	Lys	Thr	Ser	Gly	Ser
1205						1210					1215			
Arg	Thr	Pro	Gly	Arg	Tyr	Ser	Thr	Gly	Ser	Gln	Ser	Arg	Ile	Arg
1220						1225					1230			
Arg	Met	Trp	Asn	Asp	Thr	Val	Arg	Lys	Gln	Ser	Glu	Ser	Ser	Phe
1235						1240					1245			

Ile	Thr	Gly	Asp	Ile	Asn	Ser	Ser	Ala	Ser	Leu	Asn	Arg	Glu	Gly
1250						1255					1260			
Leu	Leu	Asn	Asn	Ala	Arg	Asp	Thr	Ser	Val	Met	Asp	Thr	Leu	Pro
1265						1270					1275			
Leu	Asn	Gly	Asn	His	Gly	Asn	Ser	Tyr	Ser	Ile	Ala	Gly	Gly	Glu
1280						1285					1290			
Tyr	Leu	Ser	Asn	Cys	Val	Gln	Ile	Ile	Asp	Arg	Gly	Tyr	Asn	His
1295						1300					1305			
Asn	Glu	Thr	Ala	Leu	Glu	Lys	Lys	Ile	Leu	Lys	Glu	Leu	Thr	Ser
1310						1315					1320			
Asn	Tyr	Ile	Pro	Ser	Tyr	Leu	Asn	Asn	His	Glu	Arg	Ser	Ser	Glu
1325						1330					1335			
Gln	Asn	Arg	Asn	Met	Met	Asn	Lys	Leu	Val	Asp	Asn	Leu	Gly	Ser
1340						1345					1350			
Gly	Ser	Glu	Asp	Asp	Ala	Ile	Val	Leu	Asp	Asp	Ala	Ala	Ser	Phe
1355						1360					1365			
Asn	His	Glu	Glu	Ser	Leu	Gly	Leu	Glu	Leu	Ile	His	Glu	Glu	Ser
1370						1375					1380			
Asp	Ala	Pro	Leu	Leu	Pro	Pro	Arg	Val	Tyr	Ser	Thr	Asp	Asn	His
1385						1390					1395			
Gln	Pro	His	His	Tyr	Ser	Arg	Arg	Arg	Leu	Pro	Gln	Asp	His	Ser
1400						1405					1410			
Glu	Ser	Phe	Phe	Pro	Leu	Leu	Thr	Asp	Glu	His	Thr	Glu	Asp	Pro
1415						1420					1425			
Gln	Ser	Pro	His	Arg	Asp	Ser	Leu	Tyr	Thr	Ser	Met	Pro	Ala	Leu
1430						1435					1440			
Ala	Gly	Val	Pro	Ala	Ala	Asp	Ser	Val	Thr	Thr	Ser	Thr	Gln	Thr
1445						1450					1455			

Glu Ala Ala Ala Ala Lys Gly Gly Asp Ala Glu Asp Val Tyr Tyr
 1460 1465 1470

Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Pro Leu
 1475 1480 1485

His Ala Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
 1490 1495 1500

Val Pro Pro Asn Lys Asp Gly Ala Ser Pro Glu Gly Thr Ser Lys
 1505 1510 1515

Gly Pro Ala His Leu Val Thr Ser Leu
 1520 1525

<210> 10
 <211> 541
 <212> PRT
 <213> HUMAN

<400> 10

Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu Ala Ser Val Ile Leu
 1 5 10 15

Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu Asp Ser Val Leu Val
 20 25 30

Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly Leu Phe Gln Asp
 35 40 45

Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
 50 55 60

Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
 65 70 75 80

Ile Lys His Thr Arg Thr Gln Glu Val His His Pro Ile Cys Ala Phe
 85 90 95

Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly
 100 105 110

Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys
 115 120 125

Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu Pro Arg Ser Ala
 130 135 140

Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr Phe Ile Ser Tyr
 145 150 155 160

Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala Thr Leu Leu Thr
 165 170 175

Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu
 180 185 190

Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu
 195 200 205

Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val
 210 215 220

Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly
 225 230 235 240

Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr
 245 250 255

Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu
 260 265 270

Pro Ala Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu
 275 280 285

Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys
 290 295 300

Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr Cys Ala Gly Tyr Phe
 305 310 315 320

Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val
 325 330 335

Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu
 340 345 350

Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu
 355 360 365

Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile
 370 375 380

Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe
 385 390 395 400

Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn Val Gln Lys Gln Trp
 405 410 415

Arg Gln His Leu Cys Cys Gly Arg Phe Arg Leu Ala Asp Asn Ser Asp
 420 425 430

Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys Ser Ser Asp Asn Leu
 435 440 445

Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser Asn Ser Thr Tyr Leu
 450 455 460

Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe Lys Arg Asn Ser
 465 470 475 480

His Thr Asp Ser Ala Ser Met Asp Lys Ser Leu Ser Lys Leu Ala His
 485 490 495

Ala Asp Gly Asp Gln Thr Ser Ile Ile Pro Val His Gln Val Ile Asp
 500 505 510

Lys Val Lys Gly Tyr Cys Asn Ala His Ser Asp Asn Phe Tyr Lys Asn
 515 520 525

Ile Ile Met Ser Asp Thr Phe Ser His Ser Thr Lys Phe
 530 535 540

<210> 11
 <211> 1582
 <212> PRT
 <213> Caenorhabditis elegans

<400> 11

Met Ala Thr Ala Ser Thr Glu Ile Ser Glu Phe Ser Glu Ala Ile Glu

1	5	10	15
Ser Thr Phe Asp Leu Asp Phe Thr Ala His Gln Thr Glu Ile Ile Gly	20	25	30
Thr Tyr Trp Asn Leu Arg Ala Leu Leu Arg Leu His Arg Ser Leu Val	35	40	45
Ala Ile Asp His Val Ser Gln Lys Ser Phe Trp Glu Arg Tyr Asn His	50	55	60
Trp Ile Gln Leu Ser Met Leu Val Ser Asn Gln Asn Val Asn Leu Cys	65	70	75
Gln Ser Asn Ile Cys Gln Asn Gly Gly Thr Cys Leu Val Ala Ser Ser	85	90	95
Val Pro Ala Thr Ala Thr Cys Pro Lys Asn Ser Ile Tyr Tyr Met Gly	100	105	110
Ser Cys Tyr Val Phe Asp Thr Thr Leu Arg Asn Trp Asn Asp Ala Ala	115	120	125
Leu Tyr Cys Asn Asn Met Asn Ser Ala Thr Leu Pro Leu Val Glu Ser	130	135	140
Ala Glu Asp Gln Ala Phe Phe Ala Gly Tyr Leu Gln Ala Met Ile Pro	145	150	155
Ser Asn Pro Pro Ala Asp Met Arg Pro Pro Pro Asp Gly Ile Trp Thr	165	170	175
Ala Val Arg Gly Val Asn Asn Val Thr Arg Ala Ser Trp Val Tyr Tyr	180	185	190
Pro Gly Ser Phe Leu Val Thr Asp Thr Phe Trp Ala Pro Gln Glu Pro	195	200	205
Asn Ile Tyr Val Asn Tyr Asn Asp Val Cys Val Ala Leu Gln Ser Asp	210	215	220
Ser Phe Tyr Arg Glu Trp Thr Thr Ala Leu Cys Thr Ile Leu Lys Tyr	225	230	235
			240

Thr Val Cys Lys Val Ala Pro Thr Gln Ile Gln Ala Lys Tyr Val Ala
 245 250 255

Gln Cys Ser Cys Pro Asn Gly Tyr Gly Gly Gln Thr Cys Glu Thr Gln
 260 265 270

Ser Thr Thr Asn Gln Gln Ala Ser Thr Gln Arg Thr Cys Gly Ser Asn
 275 280 285

Asp Phe Gln Phe Ser Cys Pro Asn Asp Gln Thr Ile Thr Val Asp Phe
 290 295 300

Ala Ser Phe Gly Ala Gln Gly Gly Ser Ile Ile Thr Ser Pro Pro Asp
 305 310 315 320

Ala Leu Leu Gln Gln Ile Val Gln Lys Val Asn Ala Glu Thr Lys Lys
 325 330 335

Thr Val Asn Phe Trp Ile Gly Thr Pro Asn Asn Cys Gln Leu Leu Met
 340 345 350

Val Thr Gly Ser Ser Thr Ser Tyr Ser Gln Cys Pro Ser Ser Pro Ser
 355 360 365

Ser Thr Ala Asn Val Ile Cys Ser Thr Val Pro Gln Ser Thr Ala Ser
 370 375 380

Val Ser Ala Arg Pro Thr Gln Ser Ala Pro Val Asp Pro Val Ser Gln
 385 390 395 400

Thr Met Ala Arg Arg Glu Val Tyr Thr Gly Val Gln Pro Ile Ala Ser
 405 410 415

Ala Leu Gly Gly Gln Ser Lys Lys Thr Asn Arg Lys Leu Asn Asn Ile
 420 425 430

Cys Gln Thr Lys Ile Gly Ala Pro Leu Ser Leu Phe Leu Phe Ser Arg
 435 440 445

Asn Glu Val Ile Thr Gly Phe Val Cys Ile Ser Leu Ile Ser Ala Ser
 450 455 460

Pro Gln Ile Ile Tyr Tyr Leu Cys Ala Val Ser Leu Ile Cys His Pro
 465 470 475 480

Ser Val Pro Asp Ser Ile Asn Lys Pro Arg Tyr Cys Lys Lys Glu Lys
 485 490 495

Lys Asp Gly Ile Thr Tyr Glu Gln Thr Arg Ala Cys Met Leu His Glu
 500 505 510

Gln Pro Cys Pro Asp Pro Gln Asn Val Glu Gly Thr Val Thr Arg Tyr
 515 520 525

Cys Asn Cys Gln Thr Ala Lys Trp Glu Thr Pro Asp Thr Thr Asn Cys
 530 535 540

Thr His Arg Trp Val Ala Glu Met Glu Thr Ala Ile Lys Asp Asn Gln
 545 550 555 560

Pro Val Glu Asp Ile Ser Ser Thr Val Asn Arg Gln Leu Lys Ser Thr
 565 570 575

Ile Glu Arg Thr Leu Phe Gly Gly Asp Ile Thr Gly Thr Val Arg Leu
 580 585 590

Ser Asn Asp Met Leu Ser Leu Ala Arg Asn Gln Phe Ser Val Leu Asn
 595 600 605

Asp Arg Asn Leu Arg Glu Asn Lys Ala Arg Asn Phe Thr Glu Asn Leu
 610 615 620

Gly Gly Ser Gly Asp Gln Leu Leu Ser Pro Val Ala Ala Thr Val Trp
 625 630 635 640

Asp Gln Leu Ser Ser Thr Ile Arg Ile Gln His Ala Ser Lys Leu Met
 645 650 655

Ser Val Leu Glu Gln Ser Val Leu Leu Leu Gly Asp Tyr Met Thr Asp
 660 665 670

Gln Lys Leu Asn Leu Gln Tyr Ile Asn Trp Ala Met Glu Val Glu Arg
 675 680 685

Ser Glu Pro Glu Val Gln Thr Phe Gly Ala Ala Ala Ser Pro Asn Val
690 695 700

Gln Asp Asp Met Gly Met Met Arg Val Met Ala Ala Ala Pro Pro Ala
705 710 715 720

Pro Gln Pro Glu Thr Asn Thr Thr Ile Met Phe Pro Ser Leu Lys Leu
725 730 735

Ser Pro Thr Ile Thr Leu Pro Ser Ala Ser Leu Leu Ser Ser Leu Ala
740 745 750

Ser Pro Thr Pro Val Ala Gly Gly Gly Pro Ser Ile Leu Ser Ser Phe
755 760 765

Gln Asp Asp Thr Pro Val Gly Met Ala Ser Thr Pro Asn Leu Asn Arg
770 775 780

Asn Pro Val Lys Leu Gly Tyr Tyr Ala Phe Ala Gly Phe Gly Gln Leu
785 790 795 800

Leu Asn Asn Asn Asn Asp His Thr Leu Ile Asn Ser Gln Val Ile Gly
805 810 815

Ala Ser Ile Gln Asn Ala Thr Gln Ser Val Thr Leu Pro Val Asp His
820 825 830

Pro Val Thr Phe Thr Phe Gln His Leu Thr Thr Lys Gly Val Ser Asn
835 840 845

Pro Arg Cys Val Tyr Trp Asp Leu Met Glu Ser Lys Trp Ser Thr Leu
850 855 860

Gly Cys Thr Leu Ile Ala Thr Ser Ser Asn Ser Ser Gln Cys Ser Cys
865 870 875 880

Thr His Leu Thr Ser Phe Ala Ile Leu Met Asp Ile Ser Gly Gln Val
885 890 895

Gly Arg Leu Ser Gly Gly Leu Ala Ser Ala Leu Asp Val Val Ser Thr
900 905 910

Ile Gly Cys Ala Ile Ser Ile Val Cys Leu Ala Leu Ser Val Cys Val

915		920		925
Phe Thr Phe Phe Arg Asn Leu Gln Asn Val Arg Asn Ser Ile His Arg				
930		935		940
Asn Leu Cys Leu Cys Leu Leu Ile Ala Glu Leu Val Phe Val Ile Gly				
945		950		955 960
Met Asp Arg Thr Gly Asn Arg Thr Gly Cys Gly Val Val Ala Ile Leu				
	965		970	975
Leu His Tyr Phe Phe Leu Ser Ser Phe Cys Trp Met Leu Leu Glu Gly				
	980		985	990
Tyr Gln Leu Tyr Met Met Leu Ile Gln Val Phe Glu Pro Asn Arg Thr				
	995		1000	1005
Arg Ile Phe Leu Tyr Tyr Leu Phe Cys Tyr Gly Thr Pro Ala Val				
	1010		1015	1020
Val Val Ala Ile Ser Ala Gly Ile Lys Trp Glu Asp Tyr Gly Thr				
	1025		1030	1035
Asp Ser Tyr Cys Trp Ile Asp Thr Ser Thr Pro Thr Ile Trp Ala				
	1040		1045	1050
Phe Val Ala Pro Ile Ile Val Ile Ile Ala Ala Asn Ile Ile Phe				
	1055		1060	1065
Leu Leu Ile Ala Leu Lys Val Val Leu Ser Val Gln Ser Arg Asp				
	1070		1075	1080
Arg Thr Lys Trp Gly Arg Ile Ile Gly Trp Leu Lys Gly Ser Ala				
	1085		1090	1095
Thr Leu Leu Cys Leu Leu Gly Ile Thr Trp Ile Phe Gly Phe Leu				
	1100		1105	1110
Thr Ala Val Lys Gly Gly Thr Gly Thr Ala Phe Ala Trp Ile Phe				
	1115		1120	1125
Thr Ile Leu Asn Cys Thr Gln Gly Ile Phe Ile Phe Val Leu His				
	1130		1135	1140

Val	Val	Leu	Asn	Glu	Lys	Val	Arg	Ala	Ser	Ile	Val	Arg	Trp	Leu
1145						1150					1155			
Arg	Thr	Gly	Ile	Cys	Cys	Leu	Pro	Glu	Thr	Ser	Ser	Ala	Ala	Tyr
1160						1165					1170			
Asn	Ser	Arg	Ser	Phe	Leu	Ser	Ser	Arg	Gln	Arg	Ile	Leu	Asn	Met
1175						1180					1185			
Ile	Lys	Val	Asn	Gly	His	Ser	Tyr	Pro	Ser	Thr	Ala	Ser	Thr	Asp
1190						1195					1200			
Asp	Lys	Glu	Lys	Gln	Leu	Thr	Pro	Ile	Thr	Lys	Thr	Thr	Asp	Trp
1205						1210					1215			
Leu	Ser	Arg	Leu	Pro	Asn	Gln	Asp	Ser	Val	Ser	Ile	Pro	Glu	Ser
1220						1225					1230			
Asn	Phe	Asn	Asn	Leu	Asn	Gly	Thr	Leu	Glu	Asn	Ser	Asn	Leu	Asn
1235						1240					1245			
Ser	Ala	Glu	Ile	Lys	Glu	Glu	Asp	Glu	Ile	Pro	Glu	Leu	Arg	Arg
1250						1255					1260			
Arg	Val	Thr	Val	Asp	Leu	Asn	Pro	Met	Ile	Val	Ser	Asn	Asn	Glu
1265						1270					1275			
Ile	Glu	Arg	Met	Ser	His	Ala	Ser	Ser	Asp	Pro	Arg	Gly	Ser	Gln
1280						1285					1290			
Ile	Ile	Glu	Val	Thr	Ala	Val	Glu	Lys	Lys	Ala	Pro	Val	Lys	Arg
1295						1300					1305			
Ile	Lys	Phe	Pro	Leu	Gly	Ala	Lys	Gln	Ser	Glu	Arg	Gly	Ser	Gln
1310						1315					1320			
His	Arg	Thr	Lys	Ala	Lys	His	Gly	Thr	Gly	Thr	Leu	Val	Ser	Pro
1325						1330					1335			
Trp	His	Ile	Val	Thr	Ala	Ala	His	Leu	Ile	Gly	Ile	Ser	Glu	Asp
1340						1345					1350			

Pro	Leu	Pro	Asp	Cys	Asp	Thr	Gly	Asn	Leu	Arg	Glu	Ala	Tyr	Phe
1355						1360					1365			
Val	Arg	Asp	Tyr	Lys	Asn	Phe	Val	Ala	Phe	Val	Asn	Val	Thr	Cys
1370						1375					1380			
Ala	Val	Pro	Glu	Met	Cys	Lys	Gly	Leu	His	Arg	Lys	Asp	Met	Phe
1385						1390					1395			
Lys	Pro	Leu	Ala	Ile	Lys	Ser	Leu	Tyr	Ile	Arg	Lys	Gly	Tyr	Val
1400						1405					1410			
Gly	Asp	Gly	Cys	Ile	Asp	Arg	Glu	Ser	Phe	Asn	Asp	Ile	Ala	Val
1415						1420					1425			
Phe	Glu	Leu	Glu	Glu	Pro	Ile	Glu	Phe	Ser	Lys	Asp	Ile	Phe	Pro
1430						1435					1440			
Ala	Cys	Leu	Pro	Ser	Ala	Pro	Lys	Ile	Pro	Arg	Ile	Arg	Glu	Thr
1445						1450					1455			
Gly	Tyr	Lys	Leu	Phe	Gly	Tyr	Gly	Arg	Asp	Pro	Ser	Asp	Ser	Val
1460						1465					1470			
Leu	Glu	Ser	Gly	Lys	Leu	Lys	Ser	Leu	Tyr	Ser	Phe	Val	Ala	Glu
1475						1480					1485			
Cys	Ser	Asp	Asp	Phe	Pro	Tyr	Gly	Gly	Val	Tyr	Cys	Thr	Ser	Ala
1490						1495					1500			
Val	Asn	Arg	Gly	Leu	Ser	Cys	Asp	Gly	Asp	Ser	Gly	Ser	Gly	Val
1505						1510					1515			
Val	Arg	Thr	Ser	Asp	Thr	Arg	Asn	Val	Gln	Val	Leu	Val	Gly	Val
1520						1525					1530			
Leu	Ser	Ala	Gly	Met	Pro	Cys	Pro	Glu	Leu	Tyr	Asp	Thr	His	Asn
1535						1540					1545			
Arg	Gln	Arg	Gln	Gln	Arg	Arg	Gln	Leu	Thr	Gln	Glu	Thr	Asp	Leu
1550						1555					1560			

Leu Val Asp Val Ser Ala His Val Asp Phe Phe Cys Thr Cys Cys
 1565 1570 1575

Gly Met Cys Ser
 1580

<210> 12
 <211> 198
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide

<400> 12

Met Glu Thr Tyr Ser Leu Ser Leu Gly Asn Gln Ser Val Val Glu Pro
 1 5 10 15

Asn Ile Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
 20 25 30

Pro Ser Asn Val Arg Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu
 35 40 45

Val Ser Ser Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro
 50 55 60

Asp Ala Gln Thr Glu Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr
 65 70 75 80

Thr Lys Thr Cys Gly Phe Val Val Tyr Gln Asn Asp Lys Leu Phe Gln
 85 90 95

Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser
 100 105 110

Ser Lys Thr Asp Glu Asn Glu Gln Asp Gln Ser Ala Ser Val Asp Met
 115 120 125

Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu Phe Gln Leu Tyr Ser Tyr
 130 135 140

Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
 145 150 155 160

Cys Gln Lys Asp Lys Gly Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn
165 170 175

His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
180 185 190

Tyr Pro Lys Ser Leu Asp
195

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 13

Gln Ile Val Thr Arg Lys Val Arg Lys Thr
1 5 10

<210> 14
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 14

Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn
1 5 10 15

Ile Asp Phe Asp Asn Asn Asp Ile Pro Arg Thr Asp Thr Ile Asn Ile
20 25 30

Pro Asn Pro Met Cys Thr
35

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized peptide

<400> 15

Ile Arg Thr Met Lys Pro Leu Pro Arg His
1 5 10

<210> 16

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 16

Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn Asn Pro Gln Trp Glu
1 5 10 15

Leu Asp Tyr Arg Gln Glu Lys Ile Cys Trp Leu Ala Ile Pro Glu Pro
20 25 30

Asn Gly Val Ile Lys Ser Pro Leu Leu
35 40

<210> 17

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 17

Thr Ile Ser Ile Lys Val Leu Trp Lys Asn Asn Gln Asn Leu Thr Ser
1 5 10 15

Thr Lys Lys Val Ser Ser Met Lys Lys
20 25

<210> 18

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide

<400> 18

Asn Asp Asp Ser Ile Arg


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1                5

<210>  19
<211>  78
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthesized peptide

<400>  19

Tyr Thr Val Arg Thr Lys Val Phe Gln Ser Glu Ala Ser Lys Val Leu
1                5                10                15

Met Leu Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr
                20                25                30

Arg Pro Arg Leu Arg Val Lys Met Tyr Asn Phe Leu Arg Ser Leu Pro
                35                40                45

Thr Leu His Glu Arg Phe Arg Leu Leu Glu Thr Ser Pro Ser Thr Glu
                50                55                60

Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys Glu Ser Ile
65                70                75

<210>  20
<211>  38
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HGPRBMY6 5' PRIMER

<400>  20
cgggatgcct agatgctttc ctttgcattg tcaactttc
                                     38

<210>  21
<211>  66
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  HGPRBMY6 3' FLAG TAG PRIMER

<400>  21
cggggatccc tacttgtcgt cgtcgtcctt gtagtccatg atgctttcct ttgcattgtc
                                     60
acttttc
                                     66

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<210> 22
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 <212> DNA
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 <220>
 <223> HGPRBMY6 Forward primer 383

 <400> 22
 cagacaccat taacatcccg aat 23

 <210> 23
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 <212> DNA
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 <220>
 <223> HGPRBMY6 Reverse primer 384

 <400> 23
 agaatgaaat gccgaggaag ag 22

 <210> 24
 <211> 17
 <212> DNA
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 <220>
 <223> GAPDH-F3 forward primer

 <400> 24
 agccgagcca catcgct 17

 <210> 25
 <211> 19
 <212> DNA
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 <220>
 <223> GAPDH-R1 reverse primer

 <400> 25
 gtgaccaggc gcccaatac 19

 <210> 26
 <211> 28
 <212> DNA
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 <220>
 <223> GAPDH-FVIC Taqman(R) Probe

<400> 26
caaatccggtt gactccgacc ttcacctt

28

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 27

Gln Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln
1 5 10

<210> 28
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 28

Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser Ser Lys
1 5 10

<210> 29
<211> 13
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<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 29

Ser Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn Glu
1 5 10

<210> 30
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 30

Val Asp Met Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu
1 5 10

<210> 31
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 31

Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr
1 5 10

<210> 32
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 32

Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln Tyr
1 5 10

<210> 33
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 33

Ile Phe Gln Ile Val Thr Arg Lys Val Arg Lys Thr Ser
1 5 10

<210> 34
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 34

Phe Gly Ile Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser

1 5 10

<210> 35
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 35

Tyr Leu Leu Ile Arg Thr Met Lys Pro Leu Pro Arg His
1 5 10

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 36

Met Phe Ile Thr Ile Ser Ile Lys Val Leu Trp Lys Asn
1 5 10

<210> 37
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 37

Asn Gln Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met
1 5 10

<210> 38
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 38

Gln Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met Lys
1 5 10

<210> 39
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 39

Thr Lys Lys Val Ser Ser Met Lys Lys Ile Val Ser Thr
1 5 10

<210> 40
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 40

Leu Val Asn Asp Asp Ser Ile Arg Ile Val Phe Ser Tyr
1 5 10

<210> 41
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 41

Ile Phe Ile Leu Tyr Thr Val Arg Thr Lys Val Phe Gln
1 5 10

<210> 42
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 42

Ser Leu Gly Asn Gln Ser Val Val Glu Pro Asn Ile Ala Ile
1 5 10

<210> 43
<211> 14
<212> PRT
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<220>
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<400> 43

Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro Asp
1 5 10

<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 44

Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn Glu Gln Asp
1 5 10

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 45

Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 46

Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn Ile Asp
1 5 10

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 47

Leu Arg Ser Leu Pro Thr Leu His Glu Arg Phe Arg Leu Leu
1 5 10

<210> 48
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 48

Leu Glu Thr Ser Pro Ser Thr Glu Glu Ile Thr Leu Ser Glu
1 5 10

<210> 49
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 49

Ser Thr Glu Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys
1 5 10

<210> 50
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 50

Glu Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys Glu Ser
1 5 10

<210> 51

<211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 51

 Val Thr Arg Lys Val Arg Lys Thr Ser Val Thr Trp Val Leu
 1 5 10

 <210> 52
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 52

 Asn Leu Thr Ser Thr Lys Lys Val Ser Ser Met Lys Lys Ile
 1 5 10

 <210> 53
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 53

 Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr
 1 5 10

 <210> 54
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic polypeptide

 <400> 54

 Ser Leu Ser Leu Gly Asn Gln Ser Val Val Glu Pro Asn Ile
 1 5 10

 <210> 55
 <211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 55

Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
1 5 10

<210> 56
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 56

Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr Thr Lys Thr
1 5 10

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 57

Leu Asn Met Thr Lys Asn Tyr Thr Lys Thr Cys Gly Phe Val
1 5 10

<210> 58
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 58

Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr
1 5 10

<210> 59
<211> 14
<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 59

Leu Arg Cys Arg Cys Asn His Thr Thr Asn Phe Ala Val Leu
1 5 10

<210> 60

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 60

Trp Lys Asn Asn Gln Asn Leu Thr Ser Thr Lys Lys Val Ser
1 5 10

<210> 61

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 61

Ile Phe Cys Leu Phe Asn Thr Thr Gln Gly Leu Gln Ile Phe
1 5 10

<210> 62

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic polypeptide

<400> 62

Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu Val Ser Ser Ser Thr
1 5 10 15

<210> 63

<211> 16

<212> PRT

<213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 63
 Ile Leu Ser Asn Val Gly Cys Ala Leu Ser Val Thr Gly Leu Ala Leu
 1 5 10 15

<210> 64
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 64
 Ala Leu Ser Val Thr Gly Leu Ala Leu Thr Val Ile Phe Gln Ile Val
 1 5 10 15

<210> 65
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 65
 Leu Leu Phe Val Phe Gly Ile Glu Asn Ser Asn Lys Asn Leu Gln Thr
 1 5 10 15

<210> 66
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 66
 Val Ala Ile Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn Asn Pro
 1 5 10 15

<210> 67
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<220>
<221> misc_feature
<222> (25)..(83)
<223> wherein "n" equals A, C, G, or T.

<220>
<221> misc_feature
<222> (27)..(84)
<223> wherein "k" equals C, G, or T.

<400> 67
cgaagcgtaa gggcccagcc ggcennknk nnknknknkn nkknknknkn knknknknkn 60
nnknknknkn nkknknknkn knkccgggt ccgggcggc 99

<210> 68
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthesized Oligonucleotide

<220>
<221> misc_feature
<222> (21)..(81)
<223> wherein "v" equals C, A, or G.

<220>
<221> misc_feature
<222> (22)..(83)
<223> wherein "n" equals A, C, G, or T.

<400> 68
aaaaggaaaa aagcgccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn vnngccgccc ggacccgg 98

<210> 69
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 69

Pro Gly Pro Gly Gly
1 5

<210> 70
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 70

Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 71

Ser Asp Phe Val Gly Gly Phe Trp Phe Trp Asp Ser Leu Phe Asn
1 5 10 15

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 72

Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 73
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

<400> 73

Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 74
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 74

Arg Ile Asp Ser Cys Ala Lys Tyr Phe Leu Arg Ser Cys Asp
 1 5 10

<210> 75
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 75

Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
 1 5 10 15

<210> 76
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 76

Phe Arg Val Ser Arg Val Trp Asn Pro Pro Ser Phe Asp Ser Ala
 1 5 10 15

<210> 77
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic polypeptide
 <400> 77

His Ala Tyr Val Glu Cys Asn Asp Thr Asp Cys Arg Val Trp Phe
 1 5 10 15

<210> 78
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic 5' Primer

 <400> 78
 gcagcagcgg ccgcgacata ttatccaacg ttggatgtg 39

 <210> 79
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic 3' Primer

 <400> 79
 gcagcagtcg acgatgcttt cctttgcatt gtcac 35

 <210> 80
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic 5' Primer

 <400> 80
 gcagcagcgg ccgcattggag acttattcct tgtctttgg 39

 <210> 81
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic 3' Primer

 <400> 81
 gcagcagtcg acgtacagga taaaaatttg caatccc 37

 <210> 82
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Casein Kinase II Phosphorylation Site Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> wherein "Xaa" equals either "Ser" or "Thr".

<220>
<221> MISC_FEATURE
<222> (2)..(3)
<223> wherein "Xaa" equals any naturally occurring amino acid.

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> wherein "Xaa" equals either "Asp" or "Glu".

<400> 82

Xaa Xaa Xaa Xaa
1

<210> 83
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> cAMP- and cGMP-dependent Protein Kinase Phosphorylation Site
Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> wherein "Xaa" equals either "Arg" or "Lys".

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein "Xaa" equals any naturally occurring amino acid.

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> wherein "Xaa" equals either "Ser" or "Thr".

<400> 83

Xaa Xaa Xaa Xaa
1

<210> 84
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Asparagine Glycosylation Site Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> wherein "Xaa" equals any naturally occurring amino acid except
"Pro".

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> wherein "Xaa" equals either "Ser" or "Thr".

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> wherein "Xaa" equals any naturally occurring amino acid except
"Pro".

<400> 84

Asn Xaa Xaa Xaa
1

<210> 85
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> N-myristoylation Site Consensus Sequence

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> wherein "Xaa" equals any naturally occurring amino acid except
"Glu", "Asp", "Arg", "Lys", "His", "Pro", "Phe", "Tyr", or "Trp".

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> wherein "Xaa" equals any naturally occurring amino acid.

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> wherein "Xaa" equals either "Ser" or "Thr".

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> wherein "Xaa" equals any naturally occurring amino acid except
"Pro".

<400> 85

Gly Xaa Xaa Xaa Xaa Xaa
1 5

<210> 86

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> GPCR Consensus Sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> wherein "Xaa" equals either "Gly", "Ser", "Thr", "Ala", "Leu",
"Ile", "Val", "Met", "Phe", "Tyr", "Trp", or "Cys".

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> wherein "Xaa" equals either "Gly", "Ser", "Thr", "Ala", "Asn",
"Cys", "Pro", "Asp", or "Glu".

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> wherein "Xaa" equals any naturally occurring amino acid except
"Glu", "Asp", "Pro", "Lys", "Arg", or "His".

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> wherein "Xaa" equals any naturally occurring amino acid.

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> wherein "Xaa" equals either "Leu", "Ile", "Val", "Met", "Asn",
"Gln", "Gly", or "Ala".

<220>

<221> MISC_FEATURE

<222> (7)..(8)

<223> wherein "Xaa" equals any naturally occurring amino acid.

<220>

<221> MISC_FEATURE

<222> (9)..(9)

<223> wherein "Xaa" equals either "Leu", "Ile", "Val", "Met", "Phe", or
"Thr".

<220>

<221> MISC_FEATURE
 <222> (10)..(10)
 <223> wherein "Xaa" equals either "Gly", "Ser", "Thr", "Ala", "Asn", or
 "Cys".

<220>
 <221> MISC_FEATURE
 <222> (11)..(11)
 <223> wherein "Xaa" equals either "Leu", "Ile", "Val", "Met", "Phe",
 "Tyr", "Trp", "Ser", "Thr", "Ala", or "Cys".

<220>
 <221> MISC_FEATURE
 <222> (12)..(12)
 <223> wherein "Xaa" equals either "Asp", "Glu", "Asn", or "His".

<220>
 <221> MISC_FEATURE
 <222> (14)..(14)
 <223> wherein "Xaa" equals either "Phe", "Tyr", "Trp", "Cys", "Ser", or
 "His".

<220>
 <221> MISC_FEATURE
 <222> (15)..(16)
 <223> wherein "Xaa" equals any naturally occurring amino acid.

<220>
 <221> MISC_FEATURE
 <222> (17)..(17)
 <223> wherein "Xaa" equals either "Leu", "Ile", "Val", or "Met".

<400> 86

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
 1 5 10 15

Xaa